

Sequence Comparison 'A'

ALIGNMENTS

RESULT 1

A46493
metastasis suppressor KAI1 - human
N;Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; type
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 22-Jun-1999
C;Accession: I38942; S16156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J
Science 268, 884-886, 1995
A;Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p1
A;Reference number: I38942; MUID:95273964; PMID:7754374
A;Accession: I38942
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: EMBL:U20770; NID:g806805; PIDN:AAC50133.1; PID:g806806
R;Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homolog
A;Reference number: S16156; MUID:91153380; PMID:1842498
A;Accession: S16156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <GAU>
A;Cross-references: EMBL:X53795; NID:g35832; PIDN:CAA37804.1; PID:g35833
A;Note: the authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, N
J. Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell leuk
D9, CD37, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-239,'MV',242-267 <IMA>
A;Cross-references: GB:S48196; NID:g258294; PIDN:AAB23825.1; PID:g258295
A;Experimental source: T-cell line MOLT-4
A;Note: sequence extracted from NCBI backbone (NCBIP:117149)
C;Genetics:
A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <EX1>
F;58-78/Domain: transmembrane #status predicted <TM2>
F;79-83/Domain: intracellular #status predicted <CY2>
F;84-108/Domain: transmembrane #status predicted <TM3>
F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>

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F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.3%; Score 321.5; DB 1; Length 267;
Best Local Similarity 28.2%; Pred. No. 1.8e-19;
Matches 73; Conservative 53; Mismatches 106; Indels 27; Gaps 5;

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QY      9 IIKYFLNLINGAFLVLGLLFMGPGAWLLDRNNFLTAFDENNHFIIVPISQILIGMGSSSTV 68
Db      8 VTKYFLFLFNLIFILGAVILGFGVWILADKSSFISVLQTSSSSLRMGAYVFIGVGAVTM 67

QY     69 LFCLLGYIGIHNEIRWLLIVYAVLITWTFVQVLSAFIITKKEEVQQLWHDKIDFVISE 128
Db     68 LMGLGCGIGAVNEVRCLLGLYFAPLLILIAQVTAGALFYFNMGKLKQEMGGIVTELIRD 127

QY    129 YGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKNKENSQGV-PCSC-----T 179
Db    128 YNSSREDSLQDAW---DYVQAQVKCCGWVSFYNWTDAELMNRPEVTYPCSEVKGEEDN 184

QY    180 KSTLRKWFCDLEPLNAT-----YLEGCENKISAWYNNVNLTLIGINFGLLTSEVF 228
Db    185 SLSVRKGFCEAPGNRTQSGNHPEDWPVYQEGCMEKVQAWLQENLGIILGVGVGVAIELL 244

QY    229 QVSLTVCFPFKNIKNIIHAE 247
Db    245 GMVLSICLCRH---VHSE 259

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